

# SEQUENCE LISTING

<110> Baum, Peter Robert  
Fanslow III, William C.

<120> Molecules Designated LDCAM

<130> 2873-US

<140> to be assigned--

<141> 2001-02-06

<140> PCT/US99/17905

<141> 1999-08-05

<150> 60/095,672

<151> 1998-08-07

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 1535

<212> DNA

<213> Homo sapien

<220> CDS

<221> 16..1341

<400> 1

```

gcgggccgcgc ccgac  atg gcg agt gta gtg ctg ccg agc gga tcc cag tgt  51
                   Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys
                   1                               5               10

gcg gcg gca gcg gcg gcg gcg gcg cct ccc ggg ctc cgg ctc cgg ctt  99
Ala Ala Ala Ala Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu
                   15                               20               25

ctg ctg ttg ctc ttc tcc gcc gcg gca ctg atc ccc aca ggt gat ggg  147
Leu Leu Leu Leu Phe Ser Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly
                   30                               35               40

cag aat ctg ttt acg aaa gac gtg aca gtg atc gag gga gag gtt gcg  195
Gln Asn Leu Phe Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala
                   45                               50               55               60

acc atc agt tgc caa gtc aat aag agt gac gac tct gtg att cag cta  243
Thr Ile Ser Cys Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu
                   65                               70               75

ctg aat ccc aac agg cag acc att tat ttc agg gac ttc agg cct ttg  291
Leu Asn Pro Asn Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu
                   80                               85               90

aag gac agc agg ttt cag ttg ctg aat ttt tct agc agt gaa ctc aaa  339
Lys Asp Ser Arg Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys
                   95                               100              105

gta tca ttg aca aac gtc tca att tct gat gaa gga aga tac ttt tgc  387
Val Ser Leu Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys
                   110                               115              120

```

cag	ctc	tat	acc	gat	ccc	cca	cag	gaa	agt	tac	acc	acc	atc	aca	gtc	435
Gln	Leu	Tyr	Thr	Asp	Pro	Pro	Gln	Glu	Ser	Tyr	Thr	Thr	Ile	Thr	Val	
125					130					135					140	
ctg	gtc	cca	cca	cgt	aat	ctg	atg	atc	gat	atc	cag	aaa	gac	act	gcg	483
Leu	Val	Pro	Pro	Arg	Asn	Leu	Met	Ile	Asp	Ile	Gln	Lys	Asp	Thr	Ala	
				145					150					155		
gtg	gaa	ggg	gag	gag	att	gaa	gtc	aac	tgc	act	gct	atg	gcc	agc	aag	531
Val	Glu	Gly	Glu	Glu	Ile	Glu	Val	Asn	Cys	Thr	Ala	Met	Ala	Ser	Lys	
			160					165					170			
cca	gcc	acg	act	atc	agg	tgg	ttc	aaa	ggg	aac	aca	gag	cta	aaa	ggc	579
Pro	Ala	Thr	Thr	Ile	Arg	Trp	Phe	Lys	Gly	Asn	Thr	Glu	Leu	Lys	Gly	
			175				180					185				
aaa	tcg	gag	gtg	gaa	gag	tgg	tca	gac	atg	tac	act	gtg	acc	agt	cag	627
Lys	Ser	Glu	Val	Glu	Glu	Trp	Ser	Asp	Met	Tyr	Thr	Val	Thr	Ser	Gln	
			190			195					200					
ctg	atg	ctg	aag	gtg	cac	aag	gag	gac	gat	ggg	gtc	cca	gtg	atc	tgc	675
Leu	Met	Leu	Lys	Val	His	Lys	Glu	Asp	Asp	Gly	Val	Pro	Val	Ile	Cys	
205					210					215					220	
cag	gtg	gag	cac	cct	gcg	gtc	act	gga	aac	ctg	cag	acc	cag	cgg	tat	723
Gln	Val	Glu	His	Pro	Ala	Val	Thr	Gly	Asn	Leu	Gln	Thr	Gln	Arg	Tyr	
				225				230						235		
cta	gaa	gta	cag	tat	aag	cct	caa	gtg	cac	att	cag	atg	act	tat	cct	771
Leu	Glu	Val	Gln	Tyr	Lys	Pro	Gln	Val	His	Ile	Gln	Met	Thr	Tyr	Pro	
			240					245					250			
cta	caa	ggc	tta	acc	cgg	gaa	ggg	gac	gcg	ctt	gag	tta	aca	tgt	gaa	819
Leu	Gln	Gly	Leu	Thr	Arg	Glu	Gly	Asp	Ala	Leu	Glu	Leu	Thr	Cys	Glu	
			255				260					265				
gcc	atc	ggg	aag	ccc	cag	cct	gtg	atg	gta	act	tgg	gtg	aga	gtc	gat	867
Ala	Ile	Gly	Lys	Pro	Gln	Pro	Val	Met	Val	Thr	Trp	Val	Arg	Val	Asp	
			270			275					280					
gat	gaa	atg	cct	caa	cac	gcc	gta	ctg	tct	ggg	ccc	aac	ctg	ttc	atc	915
Asp	Glu	Met	Pro	Gln	His	Ala	Val	Leu	Ser	Gly	Pro	Asn	Leu	Phe	Ile	
285					290					295					300	
aat	aac	cta	aac	aaa	aca	gat	aat	ggg	aca	tac	cgc	tgt	gaa	gct	tca	963
Asn	Asn	Leu	Asn	Lys	Thr	Asp	Asn	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ser	
				305				310						315		
aac	ata	gtg	ggg	aaa	gct	cac	tcg	gat	tat	atg	ctg	tat	gta	tac	gat	1011
Asn	Ile	Val	Gly	Lys	Ala	His	Ser	Asp	Tyr	Met	Leu	Tyr	Val	Tyr	Asp	
			320					325				330				
ccc	ccc	aca	act	atc	cct	ccc	aca	aca	acc	acc	acc	acc	acc	acc	acc	1059
Pro	Thr	Thr	Thr	Ile	Pro	Pro	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
			335			340						345				
acc	acc	acc	acc	acc	atc	ctt	acc	atc	atc	aca	gat	tcc	cg	gca	ggg	1107
Thr	Thr	Thr	Thr	Thr	Ile	Leu	Thr	Ile	Ile	Thr	Asp	Ser	Arg	Ala	Gly	
			350			355					360					
gaa	gaa	ggc	tcg	atc	agg	gca	gtg	gat	cat	gcc	gtg	atc	ggg	ggc	gtc	1155
Glu	Glu	Gly	Ser	Ile	Arg	Ala	Val	Asp	His	Ala	Val	Ile	Gly	Gly	Val	
365					370					375					380	
gtg	gcg	gtg	gtg	gtg	ttc	gcc	atg	ctg	tgc	ttg	ctc	atc	att	ctg	ggg	1203
Val	Ala	Val	Val	Val	Phe	Ala	Met	Leu	Cys	Leu	Leu	Ile	Ile	Leu	Gly	
				385					390					395		

cgc tat ttt gcc aga cat aaa ggt aca tac ttc act cat gaa gcc aaa 1251  
 Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys  
 400 405 410

gga gcc gat gac gca gca gac gca gac aca gct ata atc aat gca gaa 1299  
 Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 415 420 425

gga gga cag aac aac tcc gaa gaa aag aaa gag tac ttc atc 1341  
 Gly Gly Gln Asn Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile  
 430 435 440

tagatcagcc tttttgtttc aatgaggtgt ccaactggcc ctatttagat gataaagaga 1401  
 cagtgtatatt ggaacttcgc agaaattcgt gtgttttttt atgaatgggt ggaaaggtgt 1461  
 gagactggga aggcctggga tttgctgtgt aaaaaaaaaa aaaaaatggt ctttggaaag 1521  
 aaaaaagcgg ccgctttctt attctatttc aacattcagc ttaatcataa tctctaaatc 1581  
 atacatgcta tttccat 1598

<210> 2  
 <211> 442  
 <212> PRT  
 <213> Homo sapien

<400> 2

Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala Ala  
 1 5 10 15

Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu  
 20 25 30

Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe  
 35 40 45

Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys  
 50 55 60

Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn  
 65 70 75 80

Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg  
 85 90 95

Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr  
 100 105 110

Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr  
 115 120 125

Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro  
 130 135 140

Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu  
 145 150 155 160

Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr  
 165 170 175

Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val  
 180 185 190

Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys  
 195 200 205  
 Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His  
 210 215 220  
 Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln  
 225 230 235 240  
 Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu  
 245 250 255  
 Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys  
 260 265 270  
 Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro  
 275 280 285  
 Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn  
 290 295 300  
 Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly  
 305 310 315 320  
 Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr  
 325 330 335  
 Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr  
 340 345 350  
 Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Ser  
 355 360 365  
 Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val Ala Val Val  
 370 375 380  
 Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala  
 385 390 395 400  
 Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp  
 405 410 415  
 Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn  
 420 425 430  
 Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile  
 435 440

<210> 3  
 <211> 1935  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> 2..1272

<400> 3

g g c g c g c c c c a g g g c t c c g g c t c c g g c t c c t g c t g t t g c t c c t t 46  
 Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu 15  
 1 5 10  
 t c g g c c g c g c a c t g a t c c c a c a g g t g a t g g a c a g a a t c t g t t t a c t 94  
 Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe Thr



Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly Lys  
 290 295 300  
 gct cat tcg gac tat atg ctg tat gta tac gat ccc ccc aca act atc 958  
 Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr Ile  
 305 310 315  
 cct cct ccc aca aca acc acc acc act acc acc acc acc acc acc 1006  
 Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr  
 320 325 330 335  
 atc ctt acc atc atc aca gat tct cga gca ggt gaa gag ggg acc att 1054  
 Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Thr Thr  
 340 345 350  
 ggg gca gtg gac cac gca gtg att ggt ggc gtc gta gcc gtg gtg gtg 1102  
 Gly Ala Val Asp His Ala Val Ile Gly Gly Val Ala Val Val Val Val  
 355 360 365  
 ttt gcc atg cta tgc ttg ctc atc att ctg ggc cgc tat ttt gcc aga 1150  
 Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala Arg  
 370 375 380  
 cat aaa ggt aca tac ttc act cat gaa gcc aaa gga gcc gat gac gca 1198  
 His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp Ala  
 385 390 395  
 gca gac gca gac aca gct ata atc aat gca gaa gga gga cag aac aac 1246  
 Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn  
 400 405 410 415  
 tcc gaa gaa aag aaa gag tac ttc at ctatgcagc ctttttgttc 1292  
 Ser Glu Glu Lys Lys Glu Tyr Phe  
 420  
 caatgagggtg tccaactggc ctgttttagat gataaagaga cagtgtactt ggaactttcg 1352  
 agaagctcgt gtggtttttt gttttgtttt gtttttttat gagtgggtgg agagatgcga 1412  
 gactgggaag gcttgggatt tgcaatgtac aaacaaaaac aaagaatgtt ctttgaagt 1472  
 acactctgct gtttgacacc tctttttaat ctggttttta tttgctttgg gttttgggtt 1532  
 tttttgggtt tttgtttttt tcatttatat ttcttctac caagtcaaac ttgggtactt 1592  
 ggatttgggt tcggttagatt gcagaaaatt ctgtgccttg tttttcattc gtttgtgtg 1652  
 tttcttccct ctgtgccatt tatttttccc aaaatcaaat ttgttttttt cccctccca 1712  
 aacctcccat tttttggaat tgacctgctg gaattcttaa gactttctcc ctgttgccag 1772  
 tttcttttat ttgtgttaac ggtgactgct ttctgttcca aattcagttt cataaaagga 1832  
 aaaccagcac aatttagatt tcatagtcca gaatttagtg tctccatgat gcatccttct 1892  
 ctgtgtgtgt aaagatttgg gtgaagaaaa aaaaaaaaaa aaa 1935  
  
 <210> 4  
 <211> 423  
 <212> PRT  
 <213> Mus musculus  
  
 <400> 4  
 Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu Ser

1	5	10	15
Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe Thr Lys	20	25	30
Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys Gln Val	35	40	45
Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn Arg Gln	50	55	60
Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg Phe Gln	65	70	75
Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr Asn Val	85	90	95
Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr Asp Pro	100	105	110
Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro Arg Asn	115	120	125
Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu Ile	130	135	140
Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr Ile Arg	145	150	155
Trp Phe Lys Gly Asn Lys Glu Leu Lys Gly Lys Ser Glu Val Glu Glu	165	170	175
Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val His	180	185	190
Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro Ala	195	200	205
Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr Lys	210	215	220
Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr Arg	225	230	235
Glu Gly Asp Ala Phe Glu Leu Thr Cys Glu Ala Ile Gly Lys Pro Gln	245	250	255
Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro Gln His	260	265	270
Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn Lys Thr	275	280	285
Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly Lys Ala	290	295	300
His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr Ile Pro	305	310	315
Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Ile	325	330	335
Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Thr Ile Gly	340	345	350
Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val Val Phe	355	360	365

Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala Arg His  
370 375 380

Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala  
385 390 395 400

Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser  
405 410 415

Glu Glu Lys Lys Glu Tyr Phe  
420

<210> 5  
<211> 29  
<212> Oligonucleotide  
<213> Homo sapien

<400> 5  
tatgtcgaca tggcgagtgt agtgctgcc 29

<210> 6  
<211> 30  
<212> Oligonucleotide  
<213> Homo sapien

<400> 6  
atatagatct atgatccact gccctgatcg 30

<210> 7  
<211> 1820  
<212> DNA  
<213> Homo sapien

<220> CDS  
<221> 157..1452  
<222>

<400> 7  
aagcttgcca cgaggcgggtc cccacctcgg ccccggggtc cgaagcgggt cgggggcgcc 60  
ctttcggtca acatcgtagt ccacccctc cccatcccca gccccgggg attcaggctc 120  
gccagcgccc agccaggag cggccggga agcgcg atg ggg gcc cca gcc gcc 174  
Met Gly Ala Pro Ala Ala  
1 5  
tcg ctc ctg ctc ctg ctc ctg ctg ttc gcc tgc tgc tgg gcg ccc ggc 222  
Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala Cys Cys Trp Ala Pro Gly  
10 15 20  
ggg gcc aac ctc tcc cag gac gcc tac tgg cag gag cag gat ttg gag 270  
Gly Ala Asn Leu Ser Gln Asp Gly Tyr Trp Gln Glu Gln Asp Leu Glu  
25 30 35  
ctg gga act ctg gct cca ctc gac gag gcc atc agc tcc aca gtc tgg 318  
Leu Gly Thr Leu Ala Pro Leu Asp Glu Ala Ile Ser Ser Thr Val Trp  
40 45 50  
agc agc cct gac atg ctg gcc agt caa gac agc cag ccc tgg aca tct 366  
Ser Ser Pro Asp Met Leu Ala Ser Gln Asp Ser Gln Pro Trp Thr Ser



55	60	65	70	
gat gaa aca gtg gtg gct ggt ggc acc gtg gtg ctc aag tgc caa gtg	75	80		414
Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu Lys Cys Gln Val			85	
aaa gat cac gag gac tca tcc ctg caa tgg tct aac cct gct cag cag	90	95	100	462
Lys Asp His Tyr Glu Asp Ser Ser Leu Gln Trp Ser Asn Pro Ala Gln Gln				
act ctc tac ttt ggg gag aag aga gcc ctt cga gat aat cga att cag	105	110	115	510
Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp Asn Arg Ile Gln				
ctg gtt acc tct acg ccc cac gag ctc agc atc agc atc agc aat gtg	120	125	130	558
Leu Val Thr Ser Thr Pro Glu Glu Leu Ser Ile Ser Ile Ser Asn Val				
gcc ctg gca gac gag ggc gag tac acc tgc tca atc ttc act atg cct	135	140	145	606
Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile Phe Thr Met Pro			150	
gtg cga act gcc aag tcc ctc gtc act gtg cta gga att cca cag aag	155	160	165	654
Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly Ile Pro Gln Lys				
ccc atc atc act ggt tat aaa tct tca tta cgg gaa aaa gac aca gcc	170	175	180	702
Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu Lys Asp Thr Ala				
acc cta aac tgt cag tct tct ggg agc aag cct gca gcc cgg ctc acc	185	190	195	750
Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr				
tgg aga aag ggt gac caa gaa ctc cac gga gaa cca acc cgc ata cag	200	205	210	798
Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln				
gaa gat ccc aat ggt aaa acc ttc act gtc agc agc tgc gtg aca ttc	215	220	225	846
Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser Ser Val Thr Phe			230	
cag gtt acc cgg gag gat gat ggg gcg agc atc gtg tgc tct gtg aac	235	240	245	894
Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser Val Asn				
cat gaa tct cta aag gga gct gac aga tcc acc tct tct caa cgc att gaa	250	255	260	942
His Glu Ser Leu Lys Gly Ala Asp Arg Ser Ser Ser Arg Ile Gln				
gtt tta tac aca cca act gcg atg att agg cca gac cct ccc att cct	265	270	275	990
Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp Pro Pro His Pro				
cgt gag ggc cag aag ctg ttg cta cac tgt gag ggt cgc ggc aat cca	280	285	290	1038
Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly Arg Gly Asn Pro				
gtc ccc cag cag tac cta tgg gag aag gag ggc agt gtg cca ccc ctg	295	300	305	1086
Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser Val Pro Pro Leu			310	
aag atg acc cag gag agt gcc ctg atc ttc cct ttc ctc aac aag agt	315	320	325	1134
Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe Leu Asn Lys Ser				
gac agt ggc acc tac ggc tgc aca gcc acc agc aac atg ggc agc tac				1182

Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn Met Gly Ser Tyr  
 330 335 340  
 aag gcc tac tac acc ctc aat gtt aat gac ccc agt ccg gtg ccc tcc 1230  
 Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser Pro Val Pro Ser  
 345 350 355  
 tcc tcc agc acc tac cac gcc atc atc ggt ggg atc gtg gct ttc att 1278  
 Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile Val Ala Phe Ile  
 360 365 370  
 gtc ttc ctg ctg ctc atc atg ctc atc ttc ctt ggc cac tac ttg atc 1326  
 Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly His Tyr Leu Ile  
 375 380 385 390  
 cgg cac aaa gga acc tac ctg aca cat gag gca aaa ggc tcc gac gat 1374  
 Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys Gly Ser Asp Asp  
 395 400 405  
 gct cca gac gcg gac acg gcc atc atc aat gca gaa ggc ggg cag tca 1422  
 Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Phe Ser  
 410 415 420  
 gga ggg gac gac aag aag gaa tat ttc atc tagaggcgcc tgcccacttc 1472  
 Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 425 430  
 ctgcgcccc cagggggccct gtgggggactg ctggggccgt caccaacccg gaactgtaca 1532  
 gagcaacccg agggccgccc ctcccgttg ctccccagcc caccaccccc cctgtacaga 1592  
 atgtctgctt tgggtgcggt ttgtactcg gtttgggaatg gggaggaggagg agggcggggg 1652  
 gaggggaggg ttgccctcag ccctttccgt ggcttctctg catttgggtt attattattt 1712  
 ttgtaacaat cccaaatcaa atctgtctcc aggcgtggaga ggcaggagcc ctgggggtgag 1772  
 aaaagcaaaa aacaacaaaa aaaaaaaaaa aaaaattcct gcggccgc 1820  
  
 <210> 8  
 <211> 432  
 <212> PRT  
 <213> Homo sapien  
  
 <400> 8  
 Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala  
 1 5 10 15  
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Gly Tyr Trp  
 20 25 30  
 Gln Glu Gln Asp Leu Glu Leu Gly Thr Leu Ala Pro Leu Asp Glu Ala  
 35 40 45  
 Ile Ser Ser Thr Val Trp Ser Ser Pro Asp Met Leu Ala Ser Gln Asp  
 50 55 60  
 Ser Gln Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val  
 65 70 75 80  
 Val Leu Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp  
 85 90 95  
 Ser Asn Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu  
 100 105 110

Arg Asp Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser  
 115 120  
 Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys  
 130 135 140  
 Ser Ile Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val  
 145 150 155 160  
 Leu Gly Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu  
 165 170 175  
 Arg Glu Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys  
 180 185 190  
 Pro Ala Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly  
 195 200 205  
 Glu Pro Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val  
 210 215 220  
 Ser Ser Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser  
 225 230 235 240  
 Ile Val Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser  
 245 250 255  
 Thr Ser Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg  
 260 265 270  
 Pro Asp Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys  
 275 280 285  
 Glu Gly Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu  
 290 295 300  
 Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe  
 305 310 315 320  
 Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr  
 325 330 335  
 Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp  
 340 345 350  
 Pro Ser Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly  
 355 360 365  
 Gly Ile Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe  
 370 375 380  
 Leu Gly His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu  
 385 390 395 400  
 Ala Lys Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn  
 405 410 415  
 Ala Glu Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 420 425 430

<210> 9  
 <211> 1718  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> CDS  
 <222> 157..1350  
 <400> 9

aagcttgcca cgaggcggtc cccacctcgg ccccgggctc cgaagcggtc cgggggcgcc 60  
 ctttcgtgcca acatcgtagt ccaacccctc cccatcccca gcccccgggg attcaggctc 120  
 gccagcgccc agccaggagg cgggcccggga agcgcg atg ggg gcc cca gcc gcc 174  
 Met Gly Ala Pro Ala Ala  
 1 5  
 tgc ctc ctg ctc ctg ctc ctg etg ttc gcc tgc tgc tgg gcg ccc gcc 222  
 Ser Leu Leu Leu Leu Leu Leu Phe Ala Cys Cys Trp Ala Pro Gly  
 10 15 20  
 ggg gcc aac ctc tcc cag gac gac agc cag ccc tgg aca tct gat gaa 270  
 Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln Pro Trp Thr Ser Asp Glu  
 25 30 35  
 aca gtg gtg gct ggt ggc acc gtg gtg ctc aag tgc caa gtg aaa gat 318  
 Thr Val Val Ala Gly Gly Thr Val Val Leu Lys Cys Gln Val Lys Asp  
 40 45 50  
 cac gag gac tca tcc ctg caa tgg tct aac cct gct cag cag act ctc 366  
 His Glu Asp Ser Ser Leu Gln Trp Ser Asn Pro Ala Gln Gln Thr Leu  
 55 60 65 70  
 tac ttt ggg gag aag aga gcc ctt cga gat aat cga att cag ctg gtt 414  
 Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp Asn Arg Ile Gln Leu Val  
 75 80 85  
 acc tct acg ccc cac gag ctc agc atc agc atc agc aat gtg gcc ctg 462  
 Thr Ser Thr Pro His Glu Leu Ser Ile Ser Ile Ser Asn Val Ala Leu  
 90 95 100  
 gca gac gag ggc gag tac acc tgc tca atc ttc act atg cct gtg cga 510  
 Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile Phe Thr Met Pro Val Arg  
 105 110 115  
 act gcc aag tcc ctc gtc act gtg cta gga att cca cag aag ccc atc 558  
 Thr Ala Lys Ser Leu Val Thr Val Leu Gly Ile Pro Gln Lys Pro Ile  
 120 125 130  
 atc act ggt tat aaa tct tca tta cgg gaa aaa gac aca gcc acc cta 606  
 Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu Lys Asp Thr Ala Thr Leu  
 135 140 145 150  
 aac tgt cag tct tct ggg agc aag cct gca gcc cgg ctc acc tgg aga 654  
 Asn Cys Glu Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr Trp Arg  
 155 160 165  
 aag ggt gac caa gaa ctc cac gga gaa cca acc cgc ata cag gaa gat 702  
 Lys Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln Glu Asp  
 170 175 180  
 ccc aat ggt aaa acc ttc act gtc agc agc tgc gtg aca ttc cag gtt 750  
 Pro Asn Gly Lys Thr Phe Thr Val Ser Ser Ser Val Thr Phe Gln Val  
 185 190 195  
 acc cgg gag gat gat ggg gcg agc atc gtg tgc tct gtg aac cat gaa 798  
 Thr Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser Val Asn His Glu  
 200 205 210  
 tct cta aag gga gct gac aga tcc acc tct caa cgc att gaa gtt tta 846

Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser Gln Arg Ile Glu Val Leu  
 215 220 225 230  
 tac aca cca act gcg atg att agg cca gac cct ccc cat cct cgt gag 894  
 Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp Pro His Pro Arg Glu  
 235 240 245  
 ggc cag aag ctg ttg cta cac tgt gag ggt cgc ggc aat cca gtc ccc 942  
 Gly Leu Lys Leu Leu His Cys Glu Gly Arg Gly Asn Pro Val Pro  
 250 255 260  
 cag cag tac cta tgg gag aag gag ggc agt gtg cca ccc ctg aag atg 990  
 Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser Val Pro Pro Leu Lys Met  
 265 270 275  
 acc cag gag agt gcc ctg atc ttc cct ttc ctc aac aag agt gac agt 1038  
 Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe Leu Asn Lys Ser Asp Ser  
 280 285 290  
 ggc acc tac gcc tgc aca gcc acc agc aac atg ggc agc tac aag gcc 1086  
 Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn Met Gly Ser Tyr Lys Ala  
 295 300 305  
 tac tac acc ctc aat gtt aat gac ccc agt ccg gtg ccc tcc tcc tcc 1134  
 Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser Pro Val Pro Ser Ser Ser  
 315 320 325  
 agc acc tac cac gcc atc atc ggt ggg atc gtg gct ttc att gtc ttc 1182  
 Ser Thr Tyr His Ala Ile Ile Gly Gly Ile Val Ala Phe Ile Val Phe  
 330 335 340  
 ctg ctg ctc atc atg ctc atc ttc ctt ggc cac tac ttg atc cgg cac 1230  
 Leu Leu Leu Ile Met Leu Ile Phe Leu Gly His Tyr Leu Ile Arg His  
 345 350 355  
 aaa gga acc tac ctg aca cat gag gca aaa ggc tcc gac gat gct cca 1278  
 Lys Gly Thr Tyr Leu Thr His Glu Ala Lys Gly Ser Asp Asp Ala Pro  
 360 365 370  
 gac gcg gac acg gcc atc atc aat gca gaa ggc ggg cag tca gga ggg 1326  
 Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Ser Gly Gly  
 375 380 385 390  
 gac gac aag aag gaa tat ttc atc tagaggcgcc tgcccacttc ctgcgcccc 1380  
 Asp Asp Lys Lys Glu Tyr Phe Ile  
 395  
 cagggggcct gtggggactg ctggggcggt caccaccccg gactgtgaca gagcaaccgc 1440  
 agggccgccc ctcccgcttg cteccagccc caccaccccc cctgtacaga atgtctgctt 1500  
 tgggtgcggt tttgtactcg gtttgaatg gggaggaggagg agggcggggg gaggggaggg 1560  
 ttgcctcag cctttccgtg ggcttctctg catttggtt attattattt ttgtaacaat 1620  
 cccaaatcaa atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa 1680  
 aacaaacaaa aaaaaaaaaa aaaaattcct gcggcgcc 1718  
  
 <210> 10  
 <211> 398  
 <212> PRT  
 <213> Homo sapien  
  
 <400> 10

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala  
 1 5 10 15  
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
 20 25 30  
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80  
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125  
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285  
 Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300  
 Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320  
 Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335  
 Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350  
 His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys

355						360						365			
Gly	Ser	Asp	Asp	Ala	Pro	Asp	Ala	Asp	Thr	Ala	Ile	Ile	Asn	Ala	Glu
	370					375					380				
Gly	Gly	Gln	Ser	Gly	Gly	Asp	Asp	Lys	Lys	Glu	Tyr	Phe	Ile		
385					390					395					